

Rapid PCR detection of enterohemorrhagic *Escherichia coli* (EHEC) in bovine food products and feces

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Abstract

Although *Escherichia coli* (*E. coli*) O157:H7 is a major cause of foodborne illness, other types of *E. coli* can also cause illness. *E. coli* that possess the *eae* gene for attachment and effacing have the potential to cause disease. Many real-time, molecular-based assays have been developed to detect Enterohemorrhagic *E. coli* (EHEC) including *E. coli* O157:H7. However, no assay currently exists to detect the *eae* gene present in *E. coli* O157:H7 and other EHEC strains with a confirmed positive or negative result in less than 12 h.

Raw beef food products (raw ground beef and raw boneless beef) at 25 and 375 g samples and bovine fecal samples at 2 g were inoculated with 10¹, 10³, 10⁴, and 10⁵ organisms of *E. coli* O157:H7 to test the sensitivity of this assay. Fourteen different foodborne bacteria (including *E. coli* O157:H7) and 19 various *E. coli* strains, obtained from the United States Department of Agriculture-Agricultural Research Service (USDA-ARS) were tested for specificity. *E. coli* O157:H7 was detected at the level of 10¹ organisms in both 25 and 375 g samples of raw ground and raw boneless beef products as well as 2 g samples of bovine feces after pre-enrichment and concentration. None of the 14 foodborne bacteria screened for cross-reactivity was detected. All USDA *E. coli* strains confirmed to contain the *eae* gene were detected. © 2005 Elsevier Ltd. All rights reserved.

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1. Introduction

Escherichia coli (*E. coli*) O157:H7 is a major cause of foodborne illness. An estimated 73,000 cases of infection and 61 deaths occur annually in the United States, due to this bacterium (CDC). *E. coli* O157:H7 infections cause hemorrhagic colitis and are associated with hemolytic uremic syndrome [1,2]. Cattle are a natural reservoir for *E. coli* O157:H7. Every year, many people in the US [3] and developing countries [4] are infected from consuming undercooked beef. While *E. coli* O157:H7 infections have had wide publicity, other types of *E. coli* can cause similar illness, with symptoms such as bloody diarrhea, abdominal

cramps, and fever. Recent publications have shown that these other *E. coli* strains are often found in food products [5–7].

The broad group of *E. coli* known as Enterohemorrhagic *Escherichia coli* (EHEC), including *E. coli* O157:H7, contain the *eae* gene for attachment and effacing. *E. coli* possessing this gene have the potential to attach to the intestinal lining and cause foodborne illness [7,8]. *E. coli* O157:H7 is a pathogen regulated by the United States Department of Agriculture (USDA) and Food and Drug Administration (FDA), therefore, food-manufacturing plants are subject to having their products tested for *E. coli* O157:H7 contamination. However, testing for the presence of other disease causing *E. coli*, such as O111 and O26 strains, are not currently required.

Many molecular-based *E. coli* assays have been developed. Several polymerase chain reaction (PCR) [9–11], reverse transcriptase PCR (RT-PCR) [12,13], and real-time PCR [14,15] tests have been developed to detect *E. coli*

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O157:H7. However, no test used currently detects the *eae* gene and make it possible to obtain confirmation of negative or positive test results in less than 12 h from the receipt of a sample.

This article describes the development of a PCR based assay for *E. coli*, which targets the *eae* gene for attachment and effacing.

2. Materials and methods

2.1. Sample preparation

Twenty-five and 375 g samples of each raw ground beef, raw boneless beef, processed beef, and two grams of bovine fecal material were weighed into sterile whirlpak filter bags. Each sample was diluted with modified Tryptic Soy Broth (1:10; weight to volume). Novobiocin was added to each sample to a final concentration of 0.002%. Spectrophotometer absorbance of a log phase *E. coli* O157:H7 culture was measured at 600 nm. The absorbance was used to calculate the original concentration of *E. coli* O157:H7 and the desired dilution levels. All inoculation levels were verified by plating each dilution on standard methods agar, incubating 2 days at 35–37 °C, and enumerating the colonies on each plate. Raw beef food products (25 and 375 g samples) and bovine fecal samples were inoculated with 10^1 , 10^3 , 10^4 , and 10^5 organisms of *E. coli* O157:H7 to test for sensitivity. One negative (not spiked with *E. coli* O157:H7) raw beef food product (25 and 375 g samples) or bovine fecal sample was included with each batch to monitor for any initial product contamination. The samples were mechanically homogenized for 50 s and then incubated at 35–37 °C for 6 h in a shaker incubator set at 100 rpm. An aliquot of each sample (15, 50, or 2 ml from 25, 375, and 2 g samples, respectively) was then centrifuged at 2500g for 10 min. The supernatant was discarded and the remaining pelleted material was resuspended in 200 µl TE buffer (1 M; pH 7.5) and extracted using the QIAamp DNA mini kit (QIAGEN, Valencia, CA) according to the manufacturers' instructions.

Fourteen different foodborne bacteria (including *E. coli* O157:H7) and 19 various *E. coli* strains were obtained from the United States Department of Agriculture-Agricultural Research Service (USDA-ARS). These bacteria were also grown up in modified Tryptic Soy Broth and extracted using the QIAamp DNA mini kit. The samples were then screened in duplicate to determine inclusivity and exclusivity of this testing method.

2.2. PCR amplification

Oligonucleotide primers were designed to provide for the PCR amplification of a 360 bp product spanning from base 1179 to 1539 of the *eae* gene of the EHEC genome (GenBank accession no. AF081182). In addition, internal

Table 1

Oligonucleotide primers and fluorescently labeled hybridization probes specific for the *E. coli eae* gene

Primer	Sequence
Forward primer	TGGTACGGGTAATGAAAA
Reverse primer	AATAGCCTGGTAGTCTTGT
Upstream probe	CGCAGTCAGGGCGGTCAGA-FLUORESCCEIN
Downstream probe	LC RED 640-TCAGCATAGCGGAAGCCAAA-PHOSPHORYLATION

hybridization probes were designed to allow for detection of the PCR product by Fluorescence Resonance Energy Transfer (FRET) within the LightCycler (Roche). These probes anneal to the upper strand from positions 1477–1495 (upstream) and 1497–1516 (downstream). The hybridization probes are sequence specific and designed to only bind to the target DNA sequence. During the annealing step of PCR, the probes hybridize to the targeted DNA sequence. Then the fluorochrome on the 3' end of the first probe is excited by an external light source. The close proximity (1 bp) of this first fluorochrome to a second fluorochrome on 5' end of a second probe allows for the transfer of energy to take place. The second probe then emits a measurable amount of light. This measurable amount of light is proportional to the amount of product made, therefore, the progress of the reactions can be monitored during each run. The amplified product can then be slowly heated (0.1°/s), while the fluorescence is monitored. The fluorescence of the product will decrease when one of the two probes melts off of the product. This melting temperature, T_m , is specific to the targeted product. The sequences of the primers and fluorescently labeled hybridization probes are presented in Table 1.

The LightCycler DNA Master Hybridization Probes kit (Roche Diagnostics, Indianapolis, IN) was used according to the manufacturers' instructions. The amplification mixture contained the following concentrations of reactants 1 µM each primer, 0.2 µM each probe, and 3 mM MgCl. Each set of samples included a negative control (in which pcr-grade water was substituted for a sample). The amplification reactions containing 17 µl of master mix and 3 µl extracted DNA template was added to each capillary. Amplification conditions were as follows: 2 min at 95 °C; 55 cycles of 0 s at 95 °C, 5 s at 53 °C with a single fluorescence acquisition during each cycle; and 10 s at 72 °C. Melting curve conditions are as follows: 0 s at 95 °C; 15 s at 35 °C; and 0 s at 85 °C with a 0.1 C/s slope and continuous acquisition. Cooling cycle was 30 s at 40 °C.

3. Results

All 25 and 375 g samples of raw ground beef, raw boneless beef, and processed beef and the two grams samples of bovine fecal material showed amplification and detection down to the level of 10^1 *E. coli* O157:H7

Table 2

PCR amplification and melting curve analysis results for raw ground beef, raw boneless beef, and bovine fecal material spiked with *E. coli* O157:H7

Sample	Inoculum	PCR		Melting curve analysis	
		25 g	375 g	25 g	375 g
Raw ground beef	10 ¹	+	+	+	+
	10 ³	+	+	+	+
	10 ⁴	+	+	+	+
	10 ⁵	+	+	+	+
Raw boneless beef	10 ¹	+	+	+	+
	10 ³	+	+	+	+
	10 ⁴	+	+	+	+
	10 ⁵	+	+	+	+
Bovine fecal material	10 ¹	+	+	+	+
	10 ³	+	+	+	+
	10 ⁴	+	+	+	+
	10 ⁵	+	+	+	+

All samples were tested in duplicate and all yielded the same result in both tests.

organisms prior to pre-enrichment and concentration (Table 2). Fig. 1a shows the amplification of the *eae* gene of different concentrations of *E. coli* O157:H7 inoculated into 375 g samples of raw ground beef. The melting of the hybridization probes off of the amplified product produces

a drop in fluorescence, when graphed as the inverse, produce a distinctive peak at a predictable temperature, confirming the product of interest (Fig. 1b).

None of the 14 foodborne bacteria screened for cross-reactivity showed amplification except the positive control,

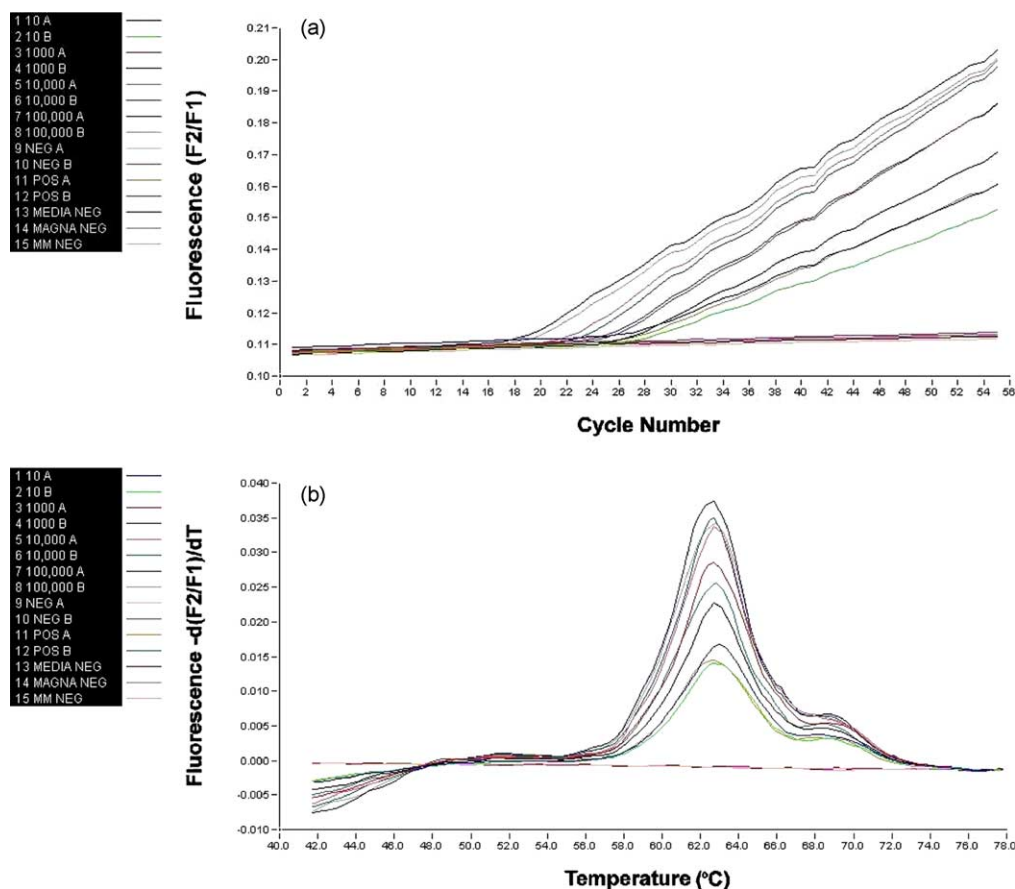


Fig. 1. The amplification (a) and melting curves (b) of the *eae* gene from different concentrations of *E. coli* O157:H7 inoculated into 375 g samples of raw ground beef. Concentrations as low as 10¹ organisms of *E. coli* O157:H7 are detectable in 375 g of raw ground beef. All samples were tested in duplicate.

Table 3
E. coli eae gene PCR inclusivity and exclusivity results

Sample ID	PCR result	Melting curve analysis
<i>Shigella flexneri</i>	—	—
<i>Listeria fermentum</i>	—	—
<i>Pantoea agglomerans</i>	—	—
<i>Enterobacter faecalis</i>	—	—
<i>Citrobacter freundii</i>	—	—
<i>Staphylococcus aureus</i> COAG +	—	—
<i>Salmonella abaeituba</i>	—	—
<i>Escherichia coli</i> O157:H7	+	+
<i>Bacillus cereus</i>	—	—
<i>Listeria monocytogenes</i>	—	—
<i>Klebsiella pneumoniae</i>	—	—
<i>Escherichia coli</i> —generic	—	—
<i>Listeria innocua</i>	—	—
<i>Escherichia vulneris</i>	—	—
USDA <i>Escherichia coli</i> isolates		
MRU-04 O145:NM	+	+
MRU-11 O145:NM	+	+
MRU-26 O145:NM	+	+
MRU-15 O157:H7	+	+
MRU-16 O157:H7	+	+
MRU-18 O157:H7	+	+
MRU-19 O157:H7	+	+
MRU-20 O157:H7	+	+
MRU-21 O157:H7	+	+
MRU-12 O157:NM	+	+
MRU-13 O157: other than H7	—	—
MRU-27 O157: other than H7	—	—
MRU-28 O157: other than H7	—	—
MRU-29 O157: other than H7	—	—
MRU-30 O55:H7	+	+
MRU-31 O55:H7	+	+
MRU-32 O55:H7	+	+
MRU-33 O55:H7	+	+
MRU-17 O55:H7	+	+

All samples were tested in duplicate and all yielded the same result in both tests.

E. coli O157:H7 isolate (Table 3). Fifteen of the 19 EHEC strains from the USDA were detected with this test (Table 3).

4. Discussion

The use of this *E. coli eae* gene detection methodology is highly sensitive, detecting as low as 10^1 organisms in 375 g of raw or processed beef.

Nineteen *E. coli* strains were obtained from the USDA for testing. After testing was completed, the USDA revealed to us that four O157: other than H7 isolates obtained from them were known not to contain the *eae* gene, but all others did contain it. All 15 isolates containing the *eae* gene obtained from the USDA tested in this study were detected. The assay proved highly specific at detecting only *E. coli* strains containing the *eae* attachment and effacing gene. Although the *sip* B-*sip* C genes in *Salmonella* and the attachment and invasion genes in *Shigella* contain

homologies to the *eae* gene in *E. coli* O157:H7 [16–18], the *Salmonella* and *Shigella* isolates tested do not cross-react with this test.

The use of hybridization probes in combination with subsequent melting curve data aids in product confirmation and could allow other primer and hybridization probe sets to be added to this assay to detect shiga-toxin producing *E. coli* genes (STEC) or other *E. coli* genes of interest. These other hybridization probes could be designed to have a different melting temperature or use a different fluorescent label than that of the *eae* gene hybridization probes.

The technique developed here for the quantitative, real-time PCR detection of EHEC dramatically reduces the reporting time compared to standard EIA, Diagnostic Culture, and other PCR methods. The method described can be used to quantify the number of genomic equivalents in each reaction with the use of standards. This assay could be used by food manufacturing plants in the future to track origins of contamination with quantification. There may even be allowable limits of contamination in some sectors of the food industry and tools like this would enable minimally contaminated lots to still be sold for certain uses.

The ability to provide *E. coli* O157:H7 test results in 12 h or less is of great benefit to food companies and the consumers of their products. Providing confirmed *E. coli* O157:H7 test results more rapidly should encourage and enable food companies to test more of their production prior to its distribution. This should reduce the amount of food products contaminated with *E. coli* O157:H7 in commerce thus reducing foodborne illness cases caused by it. More rapid turn-around time for test results will also reduce inventory and warehousing costs for food companies and provide fresher products to consumers.

5. Conclusions

The *E. coli eae* gene PCR assay described in this paper is sensitive down to 10^1 *E. coli* O157:H7 organisms in a 375 g sample. This assay can both detect and confirm the presence or absence of *E. coli* O157:H7 with great sensitivity and provide a result within 12 h upon receipt of sample. This test methodology can also detect other *E. coli* isolates containing the *eae* gene, that can cause disease, such as O111 and O26 strains or can be paired with an Immunomagnetic Separation (IMS) system to detect only *E. coli* O157:H7 in less than 12 h.

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